

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:



- (i) APPLICANT: Ceriani, Roberto L.  
Peterson, Jerry A.  
Larocca, David J.
- (ii) TITLE OF THE INVENTION: FUSION PROTEIN WITH 46 KDALTON HMFG  
DIFFERENTIATION ANTIGEN BINDING  
SPECIFICITY, COMPOSITION, KIT & METHODS
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: V. Amzel & Assoc.  
(B) STREET: P.O.Box 159  
(C) CITY: Gladwyne  
(D) STATE: Pennsylvania  
(E) COUNTRY: USA  
(F) ZIP: 19035
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk 3.5"  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
(D) SOFTWARE: PatentIn #1.0,  
Version #1.25
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/482,596  
(B) FILING DATE: June 7, 1995  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Amzel, Viviana  
(B) REGISTRATION No.: 30,930  
(C) REFERENCE/DOCKET No.: CRFC-047
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 610-649-0609  
(B) TELEFAX: 240-359-0299  
(C) TELEX: N.A.

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1384 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATTTTCATCC	ATGATGTTAA	TAAAAAACAC	AAGGAGTTTG	TGGGTAAGTG	50
GAACAAAAAC	GCGGTGCATG	TCAACCTGTT	TGAGACCCCT	GTGGAGGCTC	100
AGTACGTGAG	ATTGTACCCC	ACGAGCTGCC	ACACGGCCTG	CACTCTGCGC	150
TTTGAGCTAC	TGGGCTGTGA	GCTGAACGGA	TGCGCCAATC	CCCTGGGCCT	200

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GAAGAATAAC AGCATCCCTG ACAAGCAGAT CACGGCCTCC AGCAGCTACA 250
AGACCTGGGG CTTGCATCTC TTCAGCTGGA ACCCCTCCTA TGCACGGCTG 300
GACAAGCAGG GCAACTTCAA CGCCTGGGTT GCGGGGAGCT ACGGTAACGA 350
TCAGTGGCTG CAGGTGGACC TGGGCTCCTC GAAGGAGGTG ACAGGCATCA 400
TCACCCAGGG GGCCCGTAAC TTTGGCTCTG TCCAGTTTGT GGCATCCTAC 450
AAGGTTGCCT ACAGTAATGA CAGTGCGAAC TGGACTGAGT ACCAGGACCC 500
CAGGACTGGC AGCAGTAAGA TCTTCCCTGG CAACTGGGAC AACCCTCCC 550
ACAAGAAGAA CTTGTTTGAG ACGCCCATCC TGGCTCGCTA TGTGCGCATC 600
CTGCCTGTAG CCTGGCACAA CCGCATCGCC CTGCGCCTGG AGCTGCTGGG 650
CTGTTAGTGG CCACCTGCCA CCCCCAGGTC TTCCTGCTTT CCATGGGCCC 700
GCTGCCTCTT GGCTTCTCAG CCCCTTTAAA TCACCATAGG GCTGGGGACT 750
GGGGAAGGGG AGGGTGTTC AAGGCAGCAC CACCACACAG TCACCCCTCC 800
CTCCCTCTTT CCCACCTCC ACCTCTCACG GGCCCTGCCC CAGCCCTAA 850
GCCCCGTCCC CTAACCCCCA GTCCTCACTG TCCTGTTTTT TTAGGCACTG 900
AGGGATCTGA GTAGGTCTGG GATGGACAGG AAAGGGCAAA GTAGGGCGTG 950
TGGTTTCCCT GCCCCTGTCC GGACCGCCGA TCCCAGGTGC GTGTGTCTCT 1000
GTCTCTCCTA GCCCCTCTCT CACACATCAC ATTCCCATGG TGGCCTCAAG 1050
AAAGGCCCCG AAGCCCCAGG CTGGAGATAA CAGCCTCTTG CCCGTCGGCC 1100
CTGCGTCGGC CCTGGGGTAC CATGTGCCAC AACTGCTGTG GCCCCCTGTC 1150
CCCAAGACAC TTCCCCTTGT CTCCCTGGTT GCCTCTCTTG CCCCTTGTCC 1200
TGAAGCCCAG CGACACAGAA GGGGGTGGGG CGGGTCTATG GGGAGAAAGG 1250
GAGCGAGGTC AGAGGAGGGC ATGGGTGGGC AGGGTGGGCG TTTGGGGCCC 1300
TCATGCTGGC TTTTCACCCC AGAGGACACA GGCAGCTTCC AAAATATATT 1350
TATCTTCTTC ACGGGAAAAA AAAAAAAAAA ACCG 1384

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Asp Phe Ile His Asp Val Asn Lys Lys His Lys Glu Phe Val
 1      5      10
Gly Asn Trp Asn Lys Asn Ala Val His Val Asn Leu Phe Glu
15      20      25
Thr Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr Pro Thr Ser
30      35      40
Cys His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys
45      50      55
Glu Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn
60      65      70
Ser Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys
75      80
Thr Trp Gly Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala
85      90      95
Arg Leu Asp Lys Gln Gly Asn Phe Asn Ala Trp Val Ala Gly
100      105      110
Ser Tyr Gly Asn Asp Gln Trp Leu Gln Val Asp Leu Gly Ser
115      120      125
Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Ala Arg Asn
130      135      140
Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val Ala Tyr
145      150
Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg
155      160      165
Thr Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His
170      175      180
Ser His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg
185      190      195
Tyr Val Arg Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala
200      205      210

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Leu Arg Leu Glu Leu Leu Gly Cys  
215

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:217
- (B) TYPE:amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Phe	Ile	His	Asp	Val	Asn	Lys	Lys	His	Lys	Glu	Phe	Val	Gly
1				5					10				
Asn	Trp	Asn	Lys	Asn	Ala	Val	His	Val	Asn	Leu	Phe	Glu	Thr
15				20					25				
Pro	Val	Glu	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Thr	Ser	Cys
30				35					40				
His	Thr	Ala	Cys	Thr	Leu	Arg	Phe	Glu	Leu	Leu	Gly	Cys	Glu
			45				50					55	
Leu	Asn	Gly	Cys	Ala	Asn	Pro	Leu	Gly	Leu	Lys	Asn	Asn	Ser
			60					65					70
Ile	Pro	Asp	Lys	Gln	Ile	Thr	Ala	Ser	Ser	Ser	Tyr	Lys	Thr
			75					80					
Trp	Gly	Leu	His	Leu	Phe	Ser	Trp	Asn	Pro	Ser	Tyr	Ala	Arg
85				90					95				
Leu	Asp	Lys	Gln	Gly	Asn	Phe	Asn	Ala	Trp	Val	Ala	Gly	Ser
100				105					110				
Tyr	Gly	Asn	Asp	Gln	Trp	Leu	Gln	Val	Asp	Leu	Gly	Ser	Ser
		115		120					120				
Lys	Glu	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	Arg	Asn	Phe
			130					135					140
Gly	Ser	Val	Gln	Phe	Val	Ala	Ser	Tyr	Lys	Val	Ala	Tyr	Ser
			145					150					
Asn	Asp	Ser	Ala	Asn	Trp	Thr	Glu	Tyr	Gln	Asp	Pro	Arg	Thr
155				160					165				
Gly	Ser	Ser	Lys	Ile	Phe	Pro	Gly	Asn	Trp	Asp	Asn	His	Ser
170				175					180				
His	Lys	Lys	Asn	Leu	Phe	Glu	Thr	Pro	Ile	Leu	Ala	Arg	Tyr
		185		190					195				
Val	Arg	Ile	Leu	Pro	Val	Ala	Trp	His	Asn	Arg	Ile	Ala	Leu
		200					205						210
Arg	Leu	Glu	Leu	Leu	Gly	Cys							
			215		217								

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Phe	Lys	Gly	Asn	Ser	Thr	Arg	Asn	Val	Met	Tyr	Phe	Asn	Gly
1				5					10				
Asn	Ser	Asp	Ala	Ser	Thr	Ile	Lys	Glu	Asn	Gln	Phe	Asp	Pro
15				20					25				
Pro	Ile	Val	Ala	Arg	Tyr	Ile	Arg	Ile	Ser	Pro	Thr	Arg	Ala
30				35					40				
Tyr	Asn	Arg	Pro	Thr	Leu	Arg	Leu	Glu	Leu	Gln	Gly	Cys	Glu
		45				50						55	
Val	Asn	Gly	Cys	Ser	Thr	Pro	Leu	Gly	Met	Glu	Asn	Gly	Lys
			60					65					70
Ile	Glu	Asn	Lys	Gln	Ile	Thr	Ala	Ser	Ser	Phe	Lys	Lys	Ser
			75					80					
Trp	Trp	Gly	Asp	Tyr	Trp	Glu	Pro	Phe	Arg	Ala	Arg	Leu	Asn

85					90					95				
Ala	Gln	Gly	Arg	Val	Asn	Ala	Trp	Gln	Ala	Lys	Ala	Asn	Asn	
100					105					110				
Asn	Lys	Gln	Trp	Leu	Glu	Ile	Asp	Leu	Leu	Lys	Ile	Lys	Lys	
	115						120					125		
Ile	Thr	Ala	Ile	Ile	Thr	Gln	Gly	Cys	Lys	Ser	Leu	Ser	Ser	
	130							135				140		
Glu	Met	Tyr	Val	Lys	Ser	Tyr	Thr	Ile	His	Tyr	Ser	Glu	Gln	
			145					150						
Gly	Val	Glu	Trp	Lys	Pro	Tyr	Arg	Leu	Lys	Ser	Ser	Met	Val	
155					160					165				
Asp	Lys	Ile	Phe	Glu	Gly	Asn	Thr	Asn	Thr	Lys	Gly	His	Val	
170					175					180				
Lys	Asn	Phe	Phe	Asn	Pro	Pro	Ile	Ile	Ser	Arg	Phe	Ile	Arg	
	185					190					195			
Val	Ile	Pro	Lys	Thr	Trp	Asn	Gln	Ser	Ile	Ala	Leu	Arg	Leu	
	200						205					210		
Glu	Leu	Phe	Gly	Cys	Asp	Ile	Tyr							
				215			218							

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr	Leu	Met	Val	Phe	Phe	Gly
1				5					10				
Asn	Val	Asp	Ser	Ser	Gly	Ile	Lys	His	Asn	Ile	Phe	Asn	Pro
15					20				25				
Pro	Ile	Ile	Ala	Arg	Tyr	Ile	Arg	Leu	His	Pro	Thr	His	Tyr
	30					35				40			
Ser	Ile	Arg	Ser	Thr	Leu	Arg	Met	Glu	Leu	Met	Gly	Cys	Asp
	45					50				55			
Leu	Asn	Ser	Cys	Ser	Met	Pro	Leu	Gly	Met	Glu	Ser	Lys	Ala
	60					65				70			
Ile	Ser	Asp	Ala	Gln	Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr	Asn
	75					80				85			
Met	Phe	Ala	Thr	Trp	Ser	Pro	Ser	Lys	Ala	Arg	Leu	His	Leu
85				90				95					
Gln	Gly	Arg	Ser	Asn	Ala	Trp	Arg	Pro	Gln	Val	Asn	Asn	Pro
100					105				110				
Lys	Glu	Trp	Leu	Gln	Val	Asp	Phe	Gln	Lys	Thr	Met	Lys	Val
	115					120				125			
Thr	Gly	Val	Thr	Thr	Gln	Gly	Val	Lys	Ser	Leu	Leu	Thr	Glu
	130					135				140			
Met	Tyr	Val	Lys	Glu	Phe	Leu	Ile	Ser	Ser	Ser	Gln	Asp	Gly
			145					150					
His	Gln	Trp	Thr	Leu	Phe	Phe	Gln	Asn	Gly	Lys	Val	Lys	Val
155				160				165					
Phe	Gln	Gly	Asn	Gln	Asp	Ser	Phe	Thr	Pro	Val	Val	Asn	Ser
170					175				180				
Leu	Asp	Pro	Pro	Leu	Leu	Thr	Arg	Tyr	Leu	Arg	Ile	His	Pro
	185					190					195		
Gln	Ser	Trp	Val	His	Gln	Ile	Ala	Leu	Arg	Met	Glu	Val	Leu
	200					205					210		
Gly	Cys	Glu	Ala	Gln	Asp	Leu	Tyr						
				215			218						